



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 204874

TO: Gerald R Ewoldt
Location: rem/3C83/3C70
Art Unit: 1644
Friday, October 20, 2006
Case Serial Number: 10/620621

From: John DiNatale
Location: Biotech-Chem Library
REM-1B65
Phone: (571)272-2557

john.dinatale@uspto.gov

Search Notes

Examiner Ewoldt,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

John DiNatale
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2557

77452

10-755

204874

STIC-Biotech/ChemLib

From: Chan, Christina
 Sent: Tuesday, October 17, 2006 5:38 PM
 To: Ewoldt, Gerald; STIC-Biotech/ChemLib
 Subject: RE: RUSH Seq Search for 10/620,621

Please rush. Thanks Chris

Chris Chan
 TC 1600 New Hire Training Coordinator and SPE 1644
 (571)-272-0841
 Remsen, 3E89

-----Original Message-----

From: Ewoldt, Gerald
 Sent: Tuesday, October 17, 2006 5:22 PM
 To: Chan, Christina
 Subject: RUSH Seq Search for 10/620,621

Christina,
 Please authorize a RUSH Search.

STIC,
 Please search SEQ ID NOS:1-10 including interference and send paper copy.

Thanks,

G.R. Ewoldt, Ph.D.
 Primary Examiner
 Remsen Bldg., 3C83
 571-272-0843

1644
 3C80

1 aa 20
 2 20
 3 20
 4 19
 5 18
 6 aa 20
 7 aa 20
 8 20
 9 19
 10 aa 18

entered
 10/18

Searcher: _____
 Searcher Phone: _____
 Date Searcher Picked up: _____
 Date completed: _____
 Searcher Prep Time: _____
 Online Time: _____

Type of Search
 NA# _____ AA# _____
 S/L: _____ Oligomer: _____
 Encode/Transl: _____
 Structure #: _____ Text: _____
 Inventor: _____ Litigation: _____

Vendors and cost where applicable
 STN: _____
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
 SEQUENCE SYSTEM: _____
 WWW/Internet: _____
 Other (Specify): _____

mg

STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact:**

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen 1 A51

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 18, 2006, 19:10:59 ; Search time 93.299 Seconds
(without alignments)
98.011 Million cell updates/sec

Title: US-10-620-621-1

Perfect score: 85

Sequence: 1 TGYXXXXQSPKSLWIG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A Geneseq_8:*
- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003as:*
 - 7: geneseqp2003bs:*
 - 8: geneseqp2004s:*
 - 9: geneseqp2005s:*
 - 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	94.1	20	2 AAW05029	Synthetic
2	80	94.1	20	8 ADR14727	Adri4727 Amino aci
3	79	92.9	20	2 AAW05034	AAW05034 Synthetic
4	79	92.9	20	5 AAE27944	Aae27944 Murine 5G
5	79	92.9	20	8 ADF70140	Adf70140 Anti-idio
6	79	92.9	20	8 ADR14717	Adri4717 Synthetic
7	79	92.9	470	8 ADM72027	Adm72027 Chimeric
8	79	92.9	470	10 AEF50993	Aef50993 Variable
9	71	83.5	255	5 ABP45615	Abp45615 Human Bly
10	71	83.5	255	7 ADG96442	Adg96442 Single ch
11	71	83.5	255	9 AED78495	Aed78495 Human B L
12	71	83.5	467	9 ADZ51037	Adz51037 Amino aci
13	71	83.5	470	9 ADZ51043	Adz51043 Amino aci
14	70	82.4	97	7 ADD28121	Add28121 Lymphoma
15	68	80.0	672	6 ABP58454	Abp58454 Engineere
16	68	80.0	672	10 AEF80925	Aef80925 Staphyloc
17	65	76.5	129	5 AAU81275	Aau81275 Human trk
18	64	75.3	123	6 ABR55799	Abr55799 Heavy cha
19	64	75.3	123	6 ABR55823	Abr55823 Heavy cha
20	64	75.3	124	9 ADY96947	Ady96947 Human imm
21	64	75.3	125	9 ADZ41992	Adz41992 Ig H chai
22	64	75.3	255	5 ABP45631	Abp45631 Human Bly
23	64	75.3	255	7 ADG96458	Adg96458 Single ch

24	64	75.3	255	9 AED78511	Aed78511 Human B L
25	63	74.1	93	3 AAY64660	Aay64660 Human 5,
26	63	74.1	93	8 ADU72224	Adu72224 Signal pe
27	63	74.1	93	9 ADZ73215	Adz73215 Human inc
28	63	74.1	97	7 ADD28117	Add28117 Lymphoma
29	63	74.1	114	2 AAR79244	Aar79244 Heavy cha
30	63	74.1	114	4 AAB50793	Aab50793 Murine an
31	63	74.1	115	9 AEA34944	Aea34944 Human ant
32	63	74.1	115	9 AEB17185	Aeb17185 EphA2-spe
33	63	74.1	115	9 AEA42985	Aea42985 EphA2 ant
34	63	74.1	115	10 AEF10097	Aef10097 Mouse-hum
35	63	74.1	115	10 AEF10112	Aef10112 Mouse-hum
36	63	74.1	121	4 AAE03752	Aae03752 Murine PS
37	63	74.1	121	7 ADH44153	Adh44153 Human ant
38	63	74.1	121	9 AEB21865	Aeb21865 Human DC-
39	63	74.1	121	9 AEB21868	Aeb21868 Human DC-
40	63	74.1	121	9 AEB21864	Aeb21864 Human DC-
41	63	74.1	121	9 AEB21869	Aeb21869 Human DC-
42	63	74.1	121	9 AEB21863	Aeb21863 Human DC-
43	63	74.1	124	3 AAY87655	Aay87655 Murine PI
44	63	74.1	136	6 ABU08927	Abu08927 Mouse amy
45	63	74.1	140	3 AAY64689	Aay64689 Human 5,

ALIGNMENTS

RESULT 1

AAW05029

ID AAW05029 standard; peptide; 20 AA.

XX AC AAW05029;

XX AC AAW05029;

DT 29-MAY-1997 (first entry)

DE Synthetic peptide for treating systemic lupus erythematosus.

KW SLE; systemic lupus erythematosus; autoimmune disease; monoclonal;

KW anti-DNA antibody; CDR; complementarity determining region; 16/6 Id;

KW idiotype; nuclear antigen.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 5 /label= Met, Ala, Val

FT Misc-difference 6 /label= Gln, Asp, Glu, Arg

FT Misc-difference 7 /label= Trp, Ala

FT Misc-difference 8 /label= Val, Ser

FT Misc-difference 10 /label= Lys, Glu, Ala

PN WO9630057-Al.

PD 03-OCT-1996.

PF 27-MAR-1996; 96WO-US004206.

PR 28-MAR-1995; 95IL-00113159.

XX (YEDA) YEDA RES & DEV CO LTD.

PA (RYCU/) RYCUS A.

XX Mozes E, Waisman A;

XX WPI; 1996-455014/45.

PT New synthetic peptide(s) for treating systemic lupus erythematosus -

PT based on complementarity determining region of pathogenic anti-DNA

PT monoclonal antibody that induces SLE-like disease in mice.

XX Claim 3; Page 36; 51pp; English.

XX AAW05029-W05038 are synthetic peptides based on the complementarity-
 CC determining region (CDR) of the heavy or light chain of a pathogenic lupus
 CC Id anti-DNA monoclonal antibody (WAb), that induces a systemic lupus
 CC erythematosus (SLE)-like disease in mice. The peptides and their
 CC derivatives are used for treating SLE. The peptides inhibit or suppress
 CC specific antigen responses of SLE patients without affecting all other
 CC immune responses

XX SQ Sequence 20 AA;

Query Match 94.1%; Score 80; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYXXXXXXQSPKSLWIG 20
 |||||
 Db 1 TGYXXXXXXQSPKSLWIG 20
 |||||

RESULT 2

ADRI4727

ID ADR14727 standard; peptide; 20 AA.

XX AC ADR14727;

XX DT 21-OCT-2004 (first entry)

XX DE Amino acid sequence of a peptide used to treat SLE.

XX KW complementarity determining region; CDR; heavy chain; light chain;
 KW monoclonal anti-DNA 16/6 idioype antibody; 16/6 id antibody;
 KW anti-DNA antibody; induces systemic lupus erythematosus; SLE.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 5 /label= Met, Ala, Val

FT Misc-difference 6 /label= Gln, Asp, Glu, Arg

FT Misc-difference 7 /label= Trp, Ala

FT Misc-difference 8 /label= Val, Ser

FT Misc-difference 9 /label= Lys, Glu, Ala

XX WO2004064787-A2.

XX PD 05-AUG-2004.

XX PF 14-JAN-2004; 2004WO-US000948.

XX PR 14-JAN-2003; 2003US-0439918P.

XX PA (TEVA-) TEVA PHARM IND LTD.

XX PA (TEVA-) TEVA PHARM USA INC.

XX PI Cohen-Vered S, Naftali E, Weinstein V, Gilbert A, Klinger E;
 XX WPI; 2004-580636/56.

XX PT Pharmaceutical composition for treating systemic lupus erythematosus
 (SLE), has salt of peptide corresponding to complementarity-determining
 PT region of heavy/light chain of anti-DNA 16/6 id antibody that induces
 PT immune response to SLE.

XX PS Claim 1; SEQ ID NO 11; 132pp; English.

XX CC The specification describes a pharmaceutical composition, comprising a

CC salt of a peptide with 12-30 consecutive amino acids having a sequence
 CC corresponding to an amino acid sequence found within complementarity-
 CC determining region (CDR) of the heavy or light chain of the human
 CC monoclonal anti-DNA 16/6 idioype (16/6 Id) antibody, or a heavy or light
 CC chain of a pathogenic anti-DNA monoclonal antibody that induces systemic
 CC lupus erythematosus (SLE)-like disease response in mice. The composition
 CC is useful for treating SLE and for alleviating symptoms of SLE in a human
 CC subject. The present sequence represents a peptide which is used in
 CC pharmaceutical compositions of the invention.

XX SQ Sequence 20 AA;

Query Match 94.1%; Score 80; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYXXXXXXQSPKSLWIG 20
 |||||
 Db 1 TGYXXXXXXQSPKSLWIG 20
 |||||

RESULT 3

AAW05034

ID AAW05034 standard; peptide; 20 AA.

XX AC AAW05034;

XX DT 29-MAY-1997 (first entry)

XX DE Synthetic peptide for treating systemic lupus erythematosus.

XX KW SLE; systemic lupus erythematosus; autoimmune disease; monoclonal;
 KW anti-DNA antibody; CDR; complementarity determining region; 16/6 Id;
 KW idioype; nuclear antigen.

XX OS Synthetic.

XX PN WO9630057-A1.

XX PD 03-OCT-1996.

XX PF 27-MAR-1996; 96WO-US004206.

XX PR 28-MAR-1995; 95IL-00113159.

XX PA (YEDA) YEDA RES & DEV CO LTD.
 (RYCU/) RYCUS A.

XX PI Mozes E, Waisman A;

XX DR WPI; 1996-455014/45.

XX PT New synthetic peptide(s) for treating systemic lupus erythematosus -
 based on complementarity determining region of pathogenic anti-DNA
 PT monoclonal antibody that induces SLE-like disease in mice.

XX PS Claim 4; Page 37; 51pp; English.

XX CC AAW05029-W05038 are synthetic peptides based on the complementarity-
 CC determining region (CDR) of the heavy or light chain of a pathogenic 16/6
 CC Id anti-DNA monoclonal antibody (WAb), that induces a systemic lupus
 CC erythematosus (SLE)-like disease in mice. The peptides and their
 CC derivatives are used for treating SLE. The peptides inhibit or suppress
 CC specific antigen responses of SLE patients without affecting all other
 CC immune responses

XX SQ Sequence 20 AA;

Query Match 92.9%; Score 79; DB 2; Length 20;
 Best Local Similarity 75.0%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TGYXXXXXXQSPKSLWIG 20

XX 21-OCT-2004 (first entry)
 XX Synthetic peptide based on VH CDR1 of monoclonal antibody 5G12.
 XX complementarity determining region; CDR; heavy chain; light chain;
 XX monoclonal anti-DNA 16/6 idiotype antibody; 16/6 Id antibody;
 KW anti-DNA antibody; induces systemic lupus erythematosus; SLE;
 KW antibody 5G12.
 XX Synthetic.
 OS WO2004064787-A2.
 XX 05-AUG-2004.
 XX 14-JAN-2004; 2004WO-US000948.
 XX 14-JAN-2003; 2003US-0439918P.
 XX (TEVA-) TEVA PHARM IND LTD.
 XX (TEVA-) TEVA PHARM USA INC.
 XX Cohen-Vered S, Naftali E, Weinstein V, Gilbert A, Klinger E;
 XX WPI; 2004-580636/56.
 XX Pharmaceutical composition for treating systemic lupus erythematosus
 PT (SLE), has salt of peptide corresponding to complementarity-determining
 PT region of heavy/light chain of anti-DNA 16/6 Id antibody that induces
 PT immune response to SLE.
 XX Claim 3; SEQ ID NO 1; 132pp; English.
 XX The specification describes a pharmaceutical composition, comprising a
 CC salt of a peptide with 12-30 consecutive amino acids having a sequence
 CC corresponding to an amino acid sequence found within complementarity-
 CC determining region (CDR) of the heavy or light chain of the human
 CC monoclonal anti-DNA 16/6 idiotype (16/6 Id) antibody, or a heavy or light
 CC chain of a pathogenic anti-DNA monoclonal antibody that induces systemic
 CC lupus erythematosus (SLE)-like disease response in mice. The composition
 CC is useful for treating SLE and for alleviating symptoms of SLE in a human
 CC subject. The present sequence represents a peptide based on CDR1 of the
 CC heavy chain V region of monoclonal antibody 5G12. The 5G12 monoclonal
 CC antibody was isolated from mice with experimental SLE, and was shown to
 CC bind DNA and bear the 16/6 Id. The present peptide is used in
 CC pharmaceutical compositions of the invention.
 XX Sequence 20 AA;
 SQ
 Query Match 92.9%; Score 79; DB 8; Length 20;
 Best Local Similarity 75.0%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TGYXXXXQSPKSLWIG 20
 Db 1 TGYMQWVKQSPKSLWIG 20
 RESULT 7
 ADM72027
 ID ADM72027 standard; protein; 470 AA.
 XX ADM72027;
 XX 03-JUN-2004 (first entry)
 XX Chimeric mouse-human antibody M1E07 heavy chain.
 DE GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;
 KW cytostatic; M1E07.
 XX Mus sp.
 OS

OS Homo sapiens.
 OS Chimeric.
 XX WO2004022739-A1.
 XX 18-MAR-2004.
 PD 04-SEP-2003; 2003WO-JP011318.
 PF 04-SEP-2002; 2002WO-JP008999.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;
 XX WPI; 2004-269573/25.
 DR N-PSDB; ADM72026.
 XX Antibody against the N terminus of glypican 3 (GPC3) causes cell
 PT disruption and is useful as an anticancer agent.
 XX Example 4; SEQ ID NO 12; 122pp; Japanese.
 PS The invention relates to an antibody against the N terminus of glypican 3
 CC (GPC3). The antibody can be used for causing cell disruption and can be
 CC used as an anti-cancer agent. The present sequence represents a chimeric
 CC mouse-human antibody M1E07 heavy chain.
 XX Sequence 470 AA;
 SQ
 Query Match 92.9%; Score 79; DB 8; Length 470;
 Best Local Similarity 75.0%; Pred. No. 3.3e-05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TGYXXXXQSPKSLWIG 20
 Db 49 TGYMHVWKQSPKSLWIG 68
 RESULT 8
 AEF50993
 ID AEF50993 standard; protein; 470 AA.
 XX AEF50993;
 XX 23-MAR-2006 (first entry)
 DT Variable region of anti-glypican-3 antibody, SEQ ID NO:24.
 XX humanized antibody; antibody engineering; cell growth; cancer;
 KW cytostatic; neoplasm; hepatocellular carcinoma; gastrointestinal disease;
 KW diagnosis; glypican-3; GPC3.
 XX Mus musculus.
 OS WO2006006693-A1.
 XX 19-JAN-2006.
 PD 08-JUL-2005; 2005WO-JP013103.
 XX 09-JUL-2004; 2004JP-00203637.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Nakano K, Yoshino T, Nezu J, Tsunoda H, Igawa T, Konishi H;
 PI Tanaka M, Sugo I, Kawai S, Ishiguro T, Kinoshita Y;
 XX WPI; 2006-110188/11.
 DR Novel anti-glypican 3 antibody having high complement dependent and
 XX antibody dependent cell-mediated cytotoxicity activity with respect to
 PT cell expressing glypican 3, useful as anticancer agent and as cell growth

PT inhibitor.
 PS Disclosure; SEQ ID NO 24; 184pp; Japanese.
 XX
 CC The new invention relates to an anti-glypican 3 (GPC3) antibody (A1) comprising a heavy chain variable region having CDR1, CDR2 and CDR3 and a light chain variable region having CDR1, CDR2 and CDR3. The antibody comprises complementarity determining regions (CDRs) of amino acid sequence selected from a number of sequences fully defined in the specification. The antibody may be humanized. Also described is an antibody (A2) having an activity equivalent to (A1) and having a sequence comprising one or several amino acid substitutions, deletions, additions and/or insertions in the sequence of (A1); polynucleotide (N1) encoding the heavy-chain variable region or light-chain variable region of (A1); cell growth inhibitor (I) comprising (A1) as an active ingredient; anticancer agent (II), comprising (A1) as an active ingredient; and peptide (P1) having an amino acid sequence comprising amino acid residues 524-563, 537-563, 544-553 or 546-551 of glypican 3. (I) is useful as a cell growth inhibitor. (II) is useful as an anticancer, preferably useful for treating hepatoma. (I) is useful as an anticancer agent and as a cell growth inhibitor. (I) is useful for diagnosing cancer. (A1) has CDC and ADCC activity. The present sequence is a variable region of a murine anti-glypican-3 antibody.
 XX
 SQ Sequence 470 AA;

Query Match 92.9%; Score 79; DB 10; Length 470;
 Best Local Similarity 75.0%; Pred. No. 3.3e-05;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
 ||||| ||||| ||||| |||||
 DB 49 TGYVMHWKQSPKSLWIG 68

RESULT 9
 ABP45615
 ID ABP45615 standard; protein; 255 AA.
 AC ABP45615;

DT 19-AUG-2002 (first entry)
 DE Human Blys binding scFv SEQ ID 1626.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS
 PN WO200202641-A1.

PD 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.
 PS Claim 1; Page 2343-2344; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX

SQ Sequence 255 AA;

Query Match 83.5%; Score 71; DB 5; Length 255;
 Best Local Similarity 65.0%; Pred. No. 0.00045;
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
 :||| ||||| ||||| |||||
 DB 30 SGVYMSWVRQSPKSLWIG 49

RESULT 10
 ADG96442
 ID ADG96442 standard; protein; 255 AA.

AC ADG96442;

XX 11-MAR-2004 (first entry)

XX Single chain antibody that immunospecifically binds Blys SeqID 1626.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiaarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX Unidentified.

OS WO2003055979-A2.

PN 10-JUL-2003.

XX 14-NOV-2002; 2002WO-US036496.

PR 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 1626; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antisthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 255 AA;

Query Match 83.5%; Score 71; DB 7; Length 255;
 Best Local Similarity 65.0%; Pred. No. 0.00045;
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGYTXXXXXQSPKSLWIG 20
 :||| :||| :||| :||| :|||
 Db 30 SGYYWSWVRQSPKGLWIG 49

RESULT 11
 AED78495
 ID AED78495 standard; protein; 255 AA.

XX AED78495;

XX 12-JAN-2006 (first entry)

XX Human B Lymphocyte binding scFv fragment protein, SEQ ID 1626.

XX Antiinflammatory; Dermatological; Immunosuppressive; Antirheumatic;
 KW Antiarthritic; Neuroprotective; Muscular-Gen.; Antiaschmatic;
 KW Antiallergic; Antimicrobial; Anti-HIV; Cytostatic; B-lymphocyte;
 KW antibody; autoimmune disease; b-cell lymphoma;
 KW systemic lupus erythematosus; rheumatoid arthritis; immune disorder;
 KW inflammation; infectious disease; hyperproliferation.

XX Homo sapiens.

XX US2005255532-A1.

XX 17-NOV-2005.

XX 10-FEB-2005; 2005US-00054515.

XX 16-JUN-2000; 2000US-0212210P.

XX 17-OCT-2000; 2000US-0240818P.

XX 16-MAR-2001; 2001US-0276248P.

XX 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.

XX 15-JUN-2001; 2001US-00880748.

XX 16-NOV-2001; 2001US-0331469P.

XX 19-DEC-2001; 2001US-0340817P.

XX 14-NOV-2002; 2002US-00293418.

XX 11-FEB-2004; 2004US-0543296P.

PA (CHOI/) CHOI G H.

PA (VAUG/) VAUGHAN T.

XX (HILB/) HILBERT D.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2005-808635/82.

PT New antibodies that immunospecifically binds to B lymphocyte Stimulator

PT protein, useful for diagnosing, treating, or preventing autoimmune

PT disease, e.g. systemic lupus erythematosus or rheumatoid arthritis, or B

PT cell cancer.

XX Claim 1; SEQ ID NO 1626; 240pp; English.

XX The invention relates to a novel antibody that immunospecifically binds
 CC to a B lymphocyte Stimulator protein. The protein comprises an amino acid
 CC sequence that is 85% identical to the VH domain of any one of the single-
 CC chain variable fragments (scFvs) of SEQ ID NOS. 1-2128, and/or an amino
 CC acid sequence that is at least 85% identical to the VL domain of any one
 CC of the scFvs of SEQ ID NOS. 1-2128. The invention further comprises: an
 CC isolated nucleic acid molecule encoding the antibody; an isolated cell
 CC line that expresses the antibody; a method for detecting the expression
 CC of a B lymphocyte Stimulator protein; a method for diagnosing an
 CC autoimmune disease or a B cell cancer; and a method for treating,
 CC preventing, or ameliorating an autoimmune disease or a B cell cancer. The
 CC antibody is useful for detecting expression of B lymphocyte Stimulator
 CC protein, and in diagnosing, treating, preventing, or ameliorating an
 CC autoimmune disease or a B cell cancer. The autoimmune disease is systemic
 CC lupus erythematosus or rheumatoid arthritis. It can also be used for
 CC diagnosing, treating, and preventing immune disorders (e.g. multiple
 CC sclerosis, myasthenia gravis, or Hashimoto's disease), inflammatory
 CC disorders (e.g. asthma or allergic disorders), infectious diseases (e.g.
 CC AIDS), and proliferative disorders (e.g. leukemia, carcinoma, or
 CC lymphoma). This sequence represents a single-chain variable fragment
 CC polypeptide that immunospecifically binds to a B lymphocyte Stimulator
 CC protein of the invention. Note: This sequence is not shown in the
 CC specification. It has been electronically downloaded from the USPTO
 CC website.

XX SQ Sequence 255 AA;

Query Match 83.5%; Score 71; DB 9; Length 255;
 Best Local Similarity 65.0%; Pred. No. 0.00045;
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGYTXXXXXQSPKSLWIG 20
 :||| :||| :||| :||| :|||
 Db 30 SGYYWSWVRQSPKGLWIG 49

RESULT 12

ADZ51037

ID ADZ51037 standard; protein; 467 AA.

XX ADZ51037;

XX 30-JUN-2005 (first entry)

XX Amino acid sequence of heavy chain of anti-H4-1BB antibody.

XX antibody therapy; H4-1BB; CD137; IgG4; cytostatic; immunosuppressive;

XX antinflammatory; antimicrobial; gene therapy;

XX T cell mediated autoimmune disease; cancer; neoplasm; autoimmune disease;

XX inflammatory disease; infectious disease; heavy chain.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /note= "leader peptide"

XX WO2005035584-A1.

XX PD 21-APR-2005.
XX PF 12-OCT-2004; 2004WO-US033587.
XX XX
XX PR 10-OCT-2003; 2003US-0510193P.
XX PR 08-OCT-2004; 2004US-00961567.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Jure-Kunkel M, Hefta LJ, Santoro M, Ganguly S;
XX WPI; 2005-296269/30.
XX DR N-PSDB; ADZ51035.
XX New monoclonal antibody that specifically binds to 4-1BB comprises a
PT light chain variable region and a heavy chain variable region, useful for
PT treating cancer, autoimmune diseases, inflammatory diseases, or
PT infectious diseases.
XX Claim 3; SEQ ID NO 3; 92pp; English.
XX The specification describes fully human antibodies against human 4-1BB
CC (CD137) (H4-1BB). These antibodies are especially IgG4 antibodies.
CC Antibodies for human 4-1BB are useful as immuno-enhancers of an anti-
CC tumor or anti-viral immune response, or as immunomodulators of T cell
CC mediated autoimmune disease. They can also be used as diagnostic tools
CC for the detection of H4-1BB in blood or tissues of patients with cancer,
CC autoimmune, or other disease. The antibody can also be used for treating
CC cancer (prostate cancer, melanoma, or epithelial cancer), autoimmune
CC diseases (multiple sclerosis, rheumatoid arthritis, systemic lupus
CC erythematosus, or myasthenia gravis), inflammatory diseases, and
CC infectious diseases. ADZ51035, ADZ51036, and ADZ51037 represent the
CC coding strand, complementary strand, and encoded protein of a plasmid.
CC This plasmid encodes the heavy chain of an antibody of the invention.
XX Sequence 467 AA;
SQ
Query Match 83.5%; Score 71; DB 9; Length 467;
Best Local Similarity 65.0%; Pred. No. 0.00087;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 TGYVXXXXXXQSPKSLWIG 20
DB :||| ||||| |||||
49 SGYVSWIRQSPKSLWIG 68
RESULT 13
ADZ51043
ID ADZ51043 standard; protein; 470 AA.
XX AC ADZ51043;
XX 30-JUN-2005 (first entry)
XX DE Amino acid sequence of heavy chain of anti-H4-1BB antibody.
XX antibody therapy; H4-1BB; CD137; IgG4; cytostatic; immunosuppressive;
KW antinflammatory; antimicrobial; gene therapy;
KW T cell mediated autoimmune disease; cancer; neoplasm; autoimmune disease;
KW inflammatory disease; infectious disease; heavy chain.
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Peptide 1..19
FT /note= "leader peptide"
XX WO2005035584-A1.
XX 21-APR-2005.
XX 12-OCT-2004; 2004WO-US033587.

XX 10-OCT-2003; 2003US-0510193P.
XX PR 08-OCT-2004; 2004US-00961567.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Jure-Kunkel M, Hefta LJ, Santoro M, Ganguly S;
XX WPI; 2005-296269/30.
XX DR N-PSDB; ADZ51041.
XX New monoclonal antibody that specifically binds to 4-1BB comprises a
PT light chain variable region and a heavy chain variable region, useful for
PT treating cancer, autoimmune diseases, inflammatory diseases, or
PT infectious diseases.
XX Example 1; SEQ ID NO 9; 92pp; English.
XX The specification describes fully human antibodies against human 4-1BB
CC (CD137) (H4-1BB). These antibodies are especially IgG4 antibodies.
CC Antibodies for human 4-1BB are useful as immuno-enhancers of an anti-
CC tumor or anti-viral immune response, or as immunomodulators of T cell
CC mediated autoimmune disease. They can also be used as diagnostic tools
CC for the detection of H4-1BB in blood or tissues of patients with cancer,
CC autoimmune, or other disease. The antibody can also be used for treating
CC cancer (prostate cancer, melanoma, or epithelial cancer), autoimmune
CC diseases (multiple sclerosis, rheumatoid arthritis, systemic lupus
CC erythematosus, or myasthenia gravis), inflammatory diseases, and
CC infectious diseases. ADZ51041, ADZ51042, and ADZ51043 represent the
CC coding strand, complementary strand, and encoded protein of a construct
CC encoding the heavy chain of an antibody of the invention.
XX Sequence 470 AA;
SQ
Query Match 83.5%; Score 71; DB 9; Length 470;
Best Local Similarity 65.0%; Pred. No. 0.00088;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 TGYVXXXXXXQSPKSLWIG 20
DB :||| ||||| |||||
49 SGYVSWIRQSPKSLWIG 68
RESULT 14
ADZ51043
ID ADZ51043 standard; protein; 97 AA.
XX AC ADZ51043;
XX 15-JAN-2004 (first entry)
XX DE Lymphoma related immunoglobulin variable region.
XX B-cell; malignant; immunoglobulin; immunoglobulin variable region;
KW Ig variable region; glycosylation site; lymphoma; B cell receptor;
KW cytostatic; gene therapy; glycosylation inhibitor;
KW non-Hodgkin's lymphoma.
XX Synthetic.
OS Homo sapiens.
XX WO2003074059-A2.
XX 12-SEP-2003.
XX 24-FEB-2003; 2003WO-GB000783.
XX 07-MAR-2002; 2002GB-00005395.
XX (CANC-) CANCER RES TECHNOLOGY LTD.
XX Zhu D, Stevenson F;
XX

DR WPI; 2003-902720/82.

XX Classifying a B-cell as malignant or normal by isolating a sequence

PT representing an Ig variable region from the B cell; detecting the

PT presence of a glycosylation site and classifying the cell as malignant or

XX normal.

XX

PS Disclosure; Fig 4; 61pp; English.

XX

CC The present invention describes a method for classifying a B-cell as

CC malignant or normal comprising: (a) isolating a sequence representing an

CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the

CC presence of a glycosylation site; and (c) classifying the cell as

CC malignant or normal on the basis of the presence or absence of a

CC glycosylation site. Also described: (1) treating a patient suffering from

CC or at risk of having lymphoma; (2) screening for substances capable of

CC inhibiting glycosylation of the Ig variable region of the B cell receptor

CC ; and (3) screening for substances (s) capable of inhibiting the

CC interaction between lectins of the type found in the germinal centre and

CC N-glycans found on the surface of Ig of lymphoma cells. (S) has

CC cytostatic activity, and can be used in gene therapy, and as a

CC glycosylation inhibitor. The method is useful in classifying a B-cell as

CC malignant or normal. The glycosylation inhibitor is useful in preparing a

CC medicament for treating non-Hodgkin's lymphoma. The present sequence

CC represents an Ig variable region sequence which is used in the

CC exemplification of the present invention.

XX

XX Sequence 97 AA;

Qy Query Match 82.4%; Score 70; DB 7; Length 97;

Best Local Similarity 68.4%; Pred. No. 0.00024;

Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GYYXXXXXQSPKSLWIG 20

Db 31 GYYWSWIRQSPKGLEWIG 49

RESULT 15

ID ABP58454 standard; protein; 672 AA.

XX

AC ABP58454;

XX

DT 14-APR-2003 (first entry)

XX

DE Engineered superantigen for human cancer therapy.

XX

KW Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;

KW cytostatic; vaccine; human; SEA/E-120; mutant; mutein.

XX

OS Homo sapiens.

OS Staphylococcus sp.

OS Synthetic.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Region 1..120

FT /note= "5T4 variable heavy chain"

FT Misc-difference 41

FT /note= "wild-type His substituted by Pro"

FT Misc-difference 44

FT /note= "wild-type Ser substituted by Gly"

FT Misc-difference 69

FT /note= "wild-type Ile substituted by Thr"

FT Misc-difference 113

FT /note= "wild-type Val substituted by Gly"

FT Region 121..222

FT /note= "C242 constant heavy chain"

FT Region 226..458

FT /note= "SEA/E-120"

FT Misc-difference 245

FT /note= "wild-type Arg substituted by Gly"

FT Misc-difference 246

FT /note= "wild-type Asn substituted by Thr"

FT Misc-difference 249

FT /note= "wild-type Ser substituted by Gly"

FT Misc-difference 252

FT /note= "wild-type Arg substituted by Lys"

FT Misc-difference 304

FT /note= "wild-type Lys substituted by Glu"

FT Misc-difference 306

FT /note= "wild-type Lys substituted by Glu"

FT Misc-difference 308

FT /note= "wild-type Lys substituted by Ser"

FT Misc-difference 309

FT /note= "wild-type Lys substituted by Ser"

FT Misc-difference 452

FT /note= "wild-type Asp substituted by Ser"

FT Region 459..565

FT /note= "5T4 variable light chain"

FT Misc-difference 469

FT /note= "wild-type Phe substituted by Ser"

FT Misc-difference 504

FT /note= "wild-type Thr substituted by Lys"

FT Misc-difference 522

FT /note= "wild-type Ile substituted by Ser"

FT Misc-difference 532

FT /note= "wild-type Phe substituted by Leu"

FT Misc-difference 536

FT /note= "wild-type Thr substituted by Ser"

FT Misc-difference 537

FT /note= "wild-type Leu substituted by Val"

FT Misc-difference 542

FT /note= "wild-type Leu substituted by Ala"

FT Region 566..672

FT /note= "C242 constant light chain"

XX

PN WO2003002143-A1.

XX

XX 09-JAN-2003.

XX

PF 19-JUN-2002; 2002WO-SE001188.

XX

PR 28-JUN-2001; 2001SE-00002327.

XX

PA (ACTI-) ACTIVE BIOTECH AB.

XX

PI Forsberg G, Brlandsson E, Antonsson P, Walse B;

XX

DR WPI; 2003-201467/19.

XX

XX Conjugate for therapy, has bacterial superantigen with a region in T-cell

PT receptor and four regions to determine binding to class II major

PT histocompatibility complex, antibody to cancer associated cell surface

PT structure.

XX

PS Claim 12; Fig 10; 102pp; English.

XX

CC The present sequence is a conjugate of a bacterial superantigen and an

CC antibody moiety, and has been designed to target and destroy cancer

CC cells. The bacterial superantigen is SEA/E-120 (see also ABP58455), which

CC was derived from staphylococcal enterotoxin E (SEE) by the incorporation

CC of the following amino acid substitutions to reduce seroreactivity whilst

CC maintaining production levels and biological activity: R20G, N21T, S24G,

CC R27K, K79E, K81E, K83S and D227S. SEA/E-120 was genetically fused to the

CC Fab moiety of the tumour reactive antibody 5T4. Substitutions were made

CC in the 5T4 sequence to obtain higher yields: in the heavy chain, H41P,

CC S44G, I69T and V113G; and in the light chain, F10S, T45K, I63S, F73L,

CC T77S, I78V and L83A. An expression vector comprising DNA encoding the

CC conjugate can be used to transform host cells for recombinant production

CC of the conjugate. The conjugate is useful for treating cancer, including

CC cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,

CC cervix and prostate (claimed)

XX

SQ Sequence 672 AA;

Query Match 80.0%; Score 68; DB 6; Length 672;
 Best Local Similarity 65.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYXXXXXQSPKXLEWIG 20
 |||||
 Db 30 TGYMHVVKQSPKXLEWIG 49
 |||||

Search completed: October 18, 2006, 19:26:43
 Job time : 95.299 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2006, 19:27:25 ; Search time 13.299 Seconds
(without alignments)
144.698 Million cell updates/sec

Title: US-10-620-621-1

Perfect score: 85

Sequence: 1 TGYXXXXXQSPKSLWIG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- PIR_80:*
- 1: pir1.*
 - 2: pir2.*
 - 3: pir3.*
 - 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	92.9	105	2 PH0978	Ig heavy chain V r
2	63	74.1	107	2 S26320	Ig heavy chain V r
3	63	74.1	108	2 PH0977	Ig heavy chain V r
4	63	74.1	120	2 A49982	Ig heavy chain V r
5	62	72.9	129	1 D2HUMA	Ig heavy chain V-I
6	61	71.8	115	2 S57464	Ig heavy chain V-J
7	60	70.6	136	2 A31933	Ig heavy chain pre
8	59	69.4	91	2 S13689	Ig heavy chain V r
9	59	69.4	97	2 S26898	Ig heavy chain V r
10	59	69.4	97	2 S26806	Ig heavy chain V r
11	59	69.4	97	2 S26805	Ig heavy chain V r
12	59	69.4	97	2 S14474	Ig heavy chain V r
13	59	69.4	98	2 S17604	Ig heavy chain V r
14	59	69.4	106	2 S37454	Ig mu chain - huma
15	59	69.4	110	2 S13688	Ig heavy chain V r
16	59	69.4	111	2 S13687	Ig heavy chain V r
17	59	69.4	112	2 S13686	Ig heavy chain V r
18	59	69.4	112	2 S13685	Ig heavy chain V r
19	59	69.4	112	2 S26319	Ig heavy chain V r
20	59	69.4	122	2 JL0047	Ig heavy chain V r
21	59	69.4	126	2 S47010	Ig heavy chain V4.
22	59	69.4	135	2 PS0057	Ig heavy chain pre
23	59	69.4	140	2 S78052	Ig heavy chain pre
24	59	69.4	140	2 A49045	Ig heavy chain V r
25	58	68.2	86	2 F34964	Ig heavy chain V-I
26	58	68.2	98	2 S26912	Ig heavy chain V r
27	58	68.2	98	2 S26938	Ig heavy chain V r
28	58	68.2	98	2 S25902	Ig heavy chain V r
29	58	68.2	98	2 S12421	Ig heavy chain V r

30	58	68.2	99	2 S26801	Ig heavy chain V r
31	58	68.2	99	2 S26807	Ig heavy chain V r
32	58	68.2	104	2 S69899	Ig heavy chain V r
33	58	68.2	109	2 PH1668	Ig heavy chain V r
34	58	68.2	110	2 PH1669	Ig heavy chain V r
35	58	68.2	116	2 S37456	Ig mu chain - huma
36	58	68.2	117	1 HVHU35	Ig heavy chain pre
37	58	68.2	117	2 S18551	Ig heavy chain V r
38	58	68.2	118	2 S32665	Ig heavy chain V r
39	58	68.2	123	2 S30530	Ig heavy chain V r
40	58	68.2	126	2 I44151	Ig heavy chain V r
41	58	68.2	129	2 S46393	Ig heavy chain V r
42	58	68.2	135	2 S49530	anti-Sm antibody V
43	58	68.2	137	2 A34903	Ig heavy chain pre
44	58	68.2	140	2 A24770	hypothetical hybri
45	57	67.1	117	1 G2MSU1	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH0978

Ig heavy chain V region (clone 17s.166) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Accession: PH0978

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH0978

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-105 <TIL>

A;Cross-references: UNIPARC:UPI0000176ACA

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 79; DB 2; Length 105;

Best Local Similarity 75.0%; Pred. No. 7.7e-07;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGYXXXXXQSPKSLWIG 20

Db 29 TGYMHVVKQSPKSLWIG 48

RESULT 2

S26320

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S26320

R;Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A;Title: Antibodies that are specific for a single amino acid interchange in a protein

A;Reference number: S26309; MUID:91341421; PMID:1908510

A;Accession: S26320

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-107 <STA>

A;Cross-references: UNIPARC:UPI0000176ADF; EMBL:X59206

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 63; DB 2; Length 107;

Best Local Similarity 65.0%; Pred. No. 0.00056;

Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYXXXXXQSPKSLWIG 20
 ||||| |||||
 Db 18 TGYVHWVKQSHVKSLEWIG 37

RESULT 3

PH0977

Ig heavy chain V region (clone 10-cl) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH0977
 J: Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J: Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH0977
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-108 <TIL>
 A:Cross-references: UNIPARC:UPI0000176AC9
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 63; DB 2; Length 108;
 Best Local Similarity 65.0%; Pred. No. 0.00056;
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGYXXXXXQSPKSLWIG 20
 ||||| |||||
 Db 30 TGYVHWVKQSHVKSLEWIG 49

RESULT 4

A49982

Ig heavy chain V region (BA7.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: A49982
 J: Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.
 J: Biol. Chem. 269, 2805-2813, 1994
 A:Title: Topology of an amiloride-binding protein.
 A:Reference number: A49982; MUID:94132051; PMID:8300613
 A:Accession: A49982
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-120 <LIN>
 A:Cross-references: UNIPARC:UPI0000114AA4; GB:L24802; NID:9452096; PIDN:AAA98740.1; PID:
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 63; DB 2; Length 120;
 Best Local Similarity 65.0%; Pred. No. 0.00063;
 Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYXXXXXQSPKSLWIG 20
 ||||| |||||
 Db 30 TGYVHWVKQSHVKSLEWIG 49

RESULT 5

D2HUWA

Ig heavy chain V-II region (Wah) - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004
 C:Accession: A02099
 R: Takahashi, N.; Tetaert, D.; Debuire, B.; Lin, L.C.; Putnam, F.W.
 Proc. Natl. Acad. Sci. U.S.A. 79, 2850-2854, 1982
 A:Title: Complete amino acid sequence of the delta heavy chain of human immunoglobulin D
 A:Reference number: A02099; MUID:82222235; PMID:6806818
 A:Accession: A02099

A:Molecule type: protein
 A:Residues: 1-129 <TAK>
 A:Cross-references: UNIPROT:P01824; UNIPARC:UPI000012CEEf
 C:Comment: This chain was isolated from an IgD myeloma protein.
 C:Genetics:
 A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 62; DB 1; Length 129;
 Best Local Similarity 60.0%; Pred. No. 0.001;
 Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TGYXXXXXQSPKSLWIG 20
 ||||| |||||
 Db 32 TGYVHWVKQSHVKSLEWIG 51

RESULT 6

S57464

Ig heavy chain V-J region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S57464
 R: Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
 Submitted to the EMBL Data Library, June 1995
 A:Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropathy
 A:Reference number: S57408
 A:Accession: S57464
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-115 <PAT>
 A:Cross-references: UNIPARC:UPI00001137AD; EMBL:X87897; NID:g871273; PIDN:CAA61148.1; P:

C:Genetics: 100/2
 A:Introns:
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 61; DB 2; Length 115;
 Best Local Similarity 61.1%; Pred. No. 0.0014;
 Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 YYYXXXXXQSPKSLWIG 20
 ||||| |||||
 Db 34 YYVTWIRQSPERGLEWIG 51

RESULT 7

A31933

Ig heavy chain precursor V region (X198) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
 C:Accession: A31933
 R: Schwager, J.; Mikoryak, C.A.; Steiner, L.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 2245-2249, 1988
 A:Title: Amino acid sequence of heavy chain from Xenopus laevis Igm deduced from cDNA
 A:Reference number: A94192; MUID:88176921; PMID:2451244
 A:Accession: A31933
 A:Molecule type: mRNA
 A:Residues: 1-136 <SCH>
 A:Cross-references: UNIPROT:P20956; UNIPARC:UPI000012CED7
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:32-114/Domain: immunoglobulin homology <IMM>

Query Match 70.6%; Score 60; DB 2; Length 136;
 Best Local Similarity 55.0%; Pred. No. 0.0025;
 Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TGYXXXXXQSPKSLWIG 20

C;Accession: S26806
R;Wang, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: UNIPARC:UPI0000116488; EMBL:Z14242; NID:G37716;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 69.4%; Score 59; DB 2; Length 97;
Best Local Similarity 55.0%; Pred. No. 0.0026;
Matches 11; Conservative 1; Mismatches 8; Indels 0;

Qy 1 TGYXXXXXQSPKSLWIG 20
:|||||
Db 30 SGYYWSWIRPPGKLEWIG 49

RESULT 11

S26805
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-
C;Accession: S26805
R;Wang, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes
A;Reference number: S26800; MUID:92201299; PMID:1348029
A;Accession: S26805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WEN>
A;Cross-references: UNIPARC:UPI0000116487; EMBL:Z14241; NID:G37714;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 69.4%; Score 59; DB 2; Length 97;
Best Local Similarity 55.0%; Pred. No. 0.0026;
Matches 11; Conservative 1; Mismatches 8; Indels 0;

Qy 1 TGYXXXXXQSPKSLWIG 20
:|||||
Db 30 SGYYWSWIRPPGKLEWIG 49

RESULT 12

S14474
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-
C;Accession: S14474
R;van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanst
submitted to the EMBL Data Library, November 1990
A;Reference number: S14474
A;Accession: S14474
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <ESU>
A;Cross-references: UNIPARC:UPI0000115EC0; EMBL:X56591; NID:G37235;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 69.4%; Score 59; DB 2; Length 97;
Best Local Similarity 55.0%; Pred. No. 0.0026;
Matches 11; Conservative 1; Mismatches 8; Indels 0;

```
QY      1 TGYXXXXXXQSPKSLWIG 20
      :||| | | | | | |
Db     30 SGYYWSWIRQPPGKGLWIG 49
```

RESULT 13

SI17604
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI17604
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: SI17230: MUID:91326098: PMID:1907718

Query Match 69.4%; Score 59; DB 2; Length 98;
Best Local Similarity 60.0%; Pred. No. 0.0026;
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYVXXXXXQSPKSLWIG 20
|||: || |||||
Db 23 TGYFMNVVKOSHGKSLWIG 42

RESULT 14

S37454
Ig mu chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37454
R/McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A/Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
A/Reference number: S37453
A/Accession: S37454
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-106 <MCI>
A/Cross-references: UNIPARC:UPI00001161BE; EMBL:X75022; NID:g404311; PIDN:CAA52930.1; PDB:1Z01
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin

```
Query Match      69.4%; Score 59; DB 2; Length 106;
Best Local Similarity 55.0%; Pred. No. 0.0028;
Matches 11: Conservative 1; Mismatches 8; Indels 0; Gaps 0;
```

Qy 1 TGYXXXXXXQSPEKSLEWIG 20
:||| | | | | |
db 8 SGYVSWIROPPEGKLEWIG 27

RESULT 15

S13688
I9 heavy chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C/Accession: S13688
R:Pennell, C.A.; Mercollino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A/Rtitle: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection
A/Reference number: S13685; MUID:89338557; PMID:2503389
A/Accession: S13688
A/Molecule type: mRNA
A/Residues: 1-110 <PEN>

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: October 18, 2006, 19:11:38 ; Search time 110.309 Seconds
(without alignments)
167.713 Million cell updates/sec

Title: US-10-620-621-1

Perfect score: 85

Sequence: 1 TGYTXXXXXQSPKSLWIG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	76.5	134	Q65ZK6_MOUSE	Q65ZK6 mus musculus
2	63	74.1	118	Q5R3X0_MOUSE	Q5R3X0 mus musculus
3	63	74.1	150	Q59733_HUMAN	Q59733 homo sapien
4	63	74.1	470	Q7TMM1_MOUSE	Q7TMM1 mus musculus
5	62	72.9	129	HV2F_HUMAN	P01824 homo sapien
6	60	70.6	100	Q6B6Z2_RABIT	Q6B6Z2 oryctolagus
7	60	70.6	136	HV01_XENLA	P20956 xenopus lae
8	59	69.4	119	Q9GYZ2_MOUSE	Q9GYZ2 mus musculus
9	59	69.4	595	Q8WUX4_HUMAN	Q8WUX4 homo sapien
10	59	69.4	597	Q6GMX5_HUMAN	Q6GMX5 homo sapien
11	59	69.4	597	Q9BQ88_HUMAN	Q9BQ88 homo sapien
12	59	69.4	597	Q9BU10_HUMAN	Q9BU10 homo sapien
13	59	69.4	625	Q96AA6_HUMAN	Q96AA6 homo sapien
14	58	68.2	116	Q7Z3Y6_HUMAN	Q7Z3Y6 homo sapien
15	58	68.2	117	HV1G_HUMAN	P23083 homo sapien
16	58	68.2	119	Q9UL94_HUMAN	Q9UL94 homo sapien
17	58	68.2	125	Q9UL95_HUMAN	Q9UL95 homo sapien
18	57	67.1	117	HV41_MOUSE	P01811 mus musculus
19	57	67.1	130	Q81ZD7_HUMAN	Q81ZD7 homo sapien
20	57	67.1	483	Q4VAB6_MOUSE	Q4VAB6 mus musculus
21	56	65.9	98	Q6B6Z0_RABIT	Q6B6Z0 oryctolagus
22	56	65.9	102	Q6B6S8_RABIT	Q6B6S8 oryctolagus
23	56	65.9	103	Q6B713_RABIT	Q6B713 oryctolagus
24	56	65.9	117	HV12_MOUSE	P01756 mus musculus
25	56	65.9	117	HV13_MOUSE	P01757 mus musculus
26	56	65.9	117	HV17_MOUSE	P01786 mus musculus
27	56	65.9	117	Q9QX93_MOUSE	Q9QX93 mus musculus
28	56	65.9	117	Q9QXFO_MOUSE	Q9QXFO mus musculus
29	56	65.9	118	HV51_MOUSE	P06330 mus musculus
30	56	65.9	146	HV2I_HUMAN	P06331 homo sapien
31	56	65.9	488	Q91WR1_MOUSE	Q91WR1 mus musculus

32	54	63.5	101	2	Q6B6W2_RABIT	Q6B6W2 oryctolagus
33	54	63.5	102	2	Q6B6U5_RABIT	Q6B6U5 oryctolagus
34	54	63.5	102	2	Q6B6U6_RABIT	Q6B6U6 oryctolagus
35	54	63.5	113	1	HV29_MOUSE	P01798 mus musculus
36	54	63.5	120	2	Q920E8_MOUSE	Q920E8 mus musculus
37	53	62.4	98	1	HV57_MOUSE	P18528 mus musculus
38	53	62.4	99	2	Q6B6U4_RABIT	Q6B6U4 oryctolagus
39	53	62.4	111	1	HV35_MOUSE	P01804 mus musculus
40	53	62.4	113	1	HV27_MOUSE	P01796 mus musculus
41	53	62.4	113	1	HV28_MOUSE	P01797 mus musculus
42	53	62.4	113	1	HV30_MOUSE	P01799 mus musculus
43	53	62.4	113	1	HV31_MOUSE	P01800 mus musculus
44	53	62.4	113	1	HV34_MOUSE	P01803 mus musculus
45	53	62.4	115	1	HV32_MOUSE	P01801 mus musculus

ALIGNMENTS

RESULT 1
Q65ZR6_MOUSE PRELIMINARY; PRT; 134 AA.
AC Q65ZR6; DT 11-OCT-2004, integrated into UniProtKB/TREMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Ab 126.33 heavy chain variable and joining regions (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91237115; PubMed=1709665;
RA Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
RT "Junctional diversity of H and L chains allows the coexpression of two mutually exclusive idiotopes (Id1104 and Id1558).";
RL J. Immunol. 146:4024-4030(1991).

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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; M74139; AAA37776.1; -; mRNA.
DR SMR; Q65ZR6; 18-134.
DR Ensembl; ENSMUSG00000057641; Mus musculus.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG.V.
DR InterPro; IPR013106; V-Bet.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;

Query Match 76.5%; Score 65; DB 2; Length 134;
Best Local Similarity 65.0%; Pred. No. 0.002;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYTXXXXXQSPKSLWIG 20
DB 47 TDYTKMKVKQSPKSLWIG 66

RESULT 2
Q5R3X0_MOUSE PRELIMINARY; PRT; 118 AA.
ID Q5R3X0_MOUSE
AC Q5R3X0;
DT 21-DEC-2004, integrated into UniProtKB/TREMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
 UNK Immunoglobulin V region.
 CHAIN 1 >129
 FT Ig heavy chain V-II region WAH.
 FT /FTID=PRO_0000059912.
 FT Ig-like.
 FT DOMAIN 1 113
 FT NON_TER 129
 FT SEQUENCE 129 AA; 14117 MW; DSD53D47ABE51319 CRC64;
 SQ

Query Match 72.9%; Score 62; DB 1; Length 129;
 Best Local Similarity 60.0%; Pred No. 0.0067;
 Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
 ||||| | | | | |
 Db 32 TGYWGWIRQPGKGLEWIG 51
 ||||| | | | | |

RESULT 6
 Q6B622 RABIT PRELIMINARY; PRT; 100 AA.
 ID Q6B622_RABIT
 AC Q6B622
 DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Immunoglobulin heavy chain variable region (Fragment).
 DE Oryctolagus cuniculus (Rabbit).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OC NCBI_TaxID=9986;
 RP (1)
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN-New Zealand;
 RC PubMed=15623575; DOI=10.1084/jem.20041849;
 RA Rhee K.-J., Jasper P.-J., Sethupathi P., Shanmugam M., Lanning D.,
 RA Knight K.L.;
 RA "Positive selection of the peripheral B cell repertoire in gut-
 RT associated lymphoid tissues.";
 RT J. Exp. Med. 201:55-62(2005).
 RL (2)
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN-New Zealand;
 RC Rhee K.-J., Jasper P.-J., Sethupathi P., Knight K.L.;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RL
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; AY676781; AAT91215.1; -; mRNA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; Ig_V.
 DR InterPro; IPR013106; V-set.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR NON_TER 1
 DR NON_TER 100
 DR SEQUENCE 100 AA; 10513 MW; 5D3FDC87553C9680 CRC64;
 SQ

Query Match 70.6%; Score 60; DB 2; Length 100;
 Best Local Similarity 55.0%; Pred. No. 0.012;
 Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
 :||| | | | | |
 Db 33 SGYCYMCVVRQAPGKGLEWIG 52
 ||||| | | | | |

RESULT 7
 HV01_XENLA STANDARD; PRT; 136 AA.
 ID HV01_XENLA
 AC P20956;

```

proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC -----
DR EMBL; BC073767; AAH73767.1; -; mRNA.
DR SMR; G6GMX5; 20-249.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
DR PROSITE; 597 AA; 65305 MW; 2AIE75F6AED85230 CRC64;
SO

```

Query Match 69.4%; Score 59; DB 2; Length 597;
Best Local Similarity 55.0%;
Matches 11; Conservative 1; Pred. No. 0.13;
Mismatched 8; Indels 0; Gaps 0;

```
Qy      1 TGYXXXXXXQSPKSLWIG 20
        :||| | | | | | |
Db     49 SGYWSWIROPFGKLEWIG 68
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RESULT	11
Q9BQB8	HUMAN PRELIMINARY; PRT; 597 AA.
ID	Q9BQB8 HUMAN PRELIMINARY; PRT; 597 AA.
AC	Q9BQB8;
DC	01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT	01-JUN-2001, sequence version 1.
DE	07-FEB-2006, entry version 27.
IGHM	protein.
GN	Name=IGHM;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
NCBI_TaxID	=9606;
[1]	
RN	NCBI_TaxID=9606;
RP	TISSUE=Muscle.
RC	TISSUE=Muscle;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strauber R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA	Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshioyuki S., Carinci P., Prange C.,
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,	
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,	
Schnurch A., Schein J.E., Jones S.J.W., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human
FT	and mouse cDNA sequences.";

Best Available Copy

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 18, 2006, 19:45:04 ; Search time 24.1237 Seconds
(without alignments)
72.568 Million cell updates/sec

Title: US-10-620-621-1

Perfect score: 85

Sequence: 1 TGYVXXXXXQSPKSLWIG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	94.1	20	US-08-913-994B-1	Sequence 1, Appli
2	79	92.9	20	US-08-913-994B-6	Sequence 6, Appli
3	65	76.5	128	US-08-202-047-21	Sequence 21, Appl
4	65	76.5	128	US-08-964-690-21	Sequence 21, Appl
5	63	74.1	93	US-09-471-276-821	Sequence 821, App
6	63	74.1	114	US-08-888-366-8	Sequence 8, Appli
7	63	74.1	114	US-09-724-409-7	Sequence 7, Appli
8	63	74.1	114	US-09-724-530-7	Sequence 7, Appli
9	63	74.1	114	US-09-328-296-7	Sequence 7, Appli
10	63	74.1	121	US-09-698-705-8	Sequence 8, Appli
11	63	74.1	124	US-09-257-069-2	Sequence 2, Appli
12	63	74.1	124	US-10-007-790-2	Sequence 2, Appli
13	63	74.1	140	US-09-471-276-850	Sequence 850, App
14	63	74.1	222	US-09-698-705-13	Sequence 13, Appl
15	63	74.1	243	US-08-230-843-4	Sequence 4, Appli
16	63	74.1	243	US-08-636-936-4	Sequence 4, Appli
17	60	70.6	116	US-08-478-039-79	Sequence 79, Appl
18	60	70.6	116	US-08-476-349A-79	Sequence 79, Appl
19	60	70.6	117	US-09-744-176A-4	Sequence 4, Appli
20	60	70.6	119	US-08-478-039-77	Sequence 77, Appl
21	60	70.6	119	US-08-476-349A-77	Sequence 77, Appl
22	60	70.6	137	US-09-674-716B-50	Sequence 50, Appl
23	59	69.4	97	US-10-194-975-40	Sequence 40, Appl
24	59	69.4	97	US-10-194-975-49	Sequence 49, Appl
25	59	69.4	97	US-10-194-975-50	Sequence 50, Appl
26	59	69.4	97	US-08-896-535-76	Sequence 76, Appli

27	59	69.4	116	2	US-08-545-809A-118	Sequence 118, App
28	59	69.4	116	2	US-09-726-219A-217	Sequence 217, App
29	59	69.4	116	2	US-09-196-522-217	Sequence 217, App
30	59	69.4	116	2	US-09-515-697-118	Sequence 118, App
31	59	69.4	116	3	US-10-072-301A-38	Sequence 38, Appl
32	59	69.4	116	3	US-10-072-301A-56	Sequence 56, Appl
33	59	69.4	117	2	US-10-432-006-5	Sequence 5, Appli
34	59	69.4	123	2	US-08-793-450-4	Sequence 4, Appli
35	59	69.4	139	2	US-09-203-768A-2	Sequence 2, Appli
36	59	69.4	250	3	US-10-072-301A-21	Sequence 21, Appl
37	59	69.4	250	3	US-10-072-301A-29	Sequence 29, Appl
38	59	69.4	472	2	US-08-793-450-8	Sequence 8, Appli
39	58	68.2	76	2	US-08-851-362D-19	Sequence 19, Appl
40	58	68.2	76	2	US-09-472-087-85	Sequence 85, Appl
41	58	68.2	98	2	US-10-194-975-1	Sequence 1, Appli
42	58	68.2	98	2	US-10-194-975-44	Sequence 44, Appl
43	58	68.2	99	2	US-10-194-975-36	Sequence 36, Appl
44	58	68.2	99	2	US-10-194-975-39	Sequence 39, Appl
45	58	68.2	99	2	US-10-330-613A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-913-994B-1
; Sequence 1, Application US/08913994B
; Patent No. 6613536
; GENERAL INFORMATION:
; APPLICANT: MOZES, Edna
; WAISMAN, Ari
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS COMPRISING THEM FOR THE TREATMENT
; OF SYSTEMIC LUPUS ERYTHEMATOSUS (SLE)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 624 Ninth Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/913,994B
; FILING DATE: 29-Sep-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04206
; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: IL 113,159
; FILING DATE: 28-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MOZES=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: /note= Xaa in position 5 is Met, Ala or Val;
; Xaa in position 6 is Gln, Asp, Glu, or Arg; Xaa in
; position 7 is Trp or Ala; Xaa in position 8 is Val or Ser;

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;
; and xaa in position 9 is Lys, Glu or Ala.
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-913-994B-1
Query Match          94.1%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGYVXXXXXQSPKSLWIG 20
Db 1 TGYVXXXXXQSPKSLWIG 20

RESULT 2
US-08-913-994B-6
; Sequence 6, Application US/08913994B
; Patent No. 6613536
; GENERAL INFORMATION:
; APPLICANT: MOZES, Edna
; WAISMAN, Ari
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS COMPRISING THEM FOR THE TREATMENT
; OF SYSTEMIC LUPUS ERYTHEMATOSUS (SLE)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 624 Ninth Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,994B
; FILING DATE: 29-Sep-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04206
; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: IL 113,159
; FILING DATE: 28-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MOZES=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-913-994B-6
Query Match          92.9%; Score 79; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 3.1e-07;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TGYVXXXXXQSPKSLWIG 20
Db 1 TGYVQVWVQSPKSLWIG 20

RESULT 3
US-08-202-047-21
; Sequence 21, Application US/08202047
; Patent No. 6033667
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= MOUSE_IIA
US-08-202-047-21
Query Match          76.5%; Score 65; DB 1; Length 128;
Best Local Similarity 65.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYVXXXXXQSPKSLWIG 20
Db 30 TDYVNVWVQSPKSLWIG 49

RESULT 4
US-08-964-690-21
; Sequence 21, Application US/08964690
; Patent No. 6033667
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
```

COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,690
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-77
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..128
OTHER INFORMATION: /label= MOUSE_IIA
US-08-964-690-21

Query Match 76.5%; Score 65; DB 2; Length 128;
Best Local Similarity 65.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYXXXXXXQSPEKSLWIG 20
Db 30 TDYNNWVQSPGKSLWIG 49

RESULT 5
US-09-471-276-821
Sequence 821, Application US/09471276
Patent No. 6822072
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert A. J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6822072
FILE REFERENCE: GENSET.025CP1
CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 09/069,047
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: Patent.pm
SEQ ID NO 821
LENGTH: 93
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -19...-1
US-09-471-276-821

Query Match 74.1%; Score 63; DB 2; Length 93;
Best Local Similarity 65.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TGYXXXXXXQSPEKSLWIG 20
Db 49 TNYWSXIRQSPGKLEWIG 68
RESULT 6
US-08-888-366-8
Sequence 8, Application US/08888366
Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-366-8

Query Match 74.1%; Score 63; DB 1; Length 114;
Best Local Similarity 65.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYXXXXXXQSPEKSLWIG 20
Db 24 TGYMHWVQSHGKSLWIG 43

RESULT 7
US-09-724-409-7


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; Sequence 7, Application US/09724409
; Patent No. 6838261
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/09/724,409
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-409-7

Query Match 74.1%; Score 63; DB 2; Length 114;
Best Local Similarity 65.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXKXQSPKSLWIG 20
   ||||| || |||||
DB 30 TGYIHWVKSHGKSLWIG 49

RESULT 8
US-09-724-530-7
; Sequence 7, Application US/09724530
; Patent No. 6843989
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/09/724,530
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-530-7

Query Match 74.1%; Score 63; DB 2; Length 114;
Best Local Similarity 65.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXKXQSPKSLWIG 20
   ||||| || |||||
DB 30 TGYIHWVKSHGKSLWIG 49

RESULT 8
US-09-724-530-7
; Sequence 7, Application US/09724530
; Patent No. 6843989
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/09/724,530
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-530-7

Query Match 74.1%; Score 63; DB 2; Length 114;
Best Local Similarity 65.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXKXQSPKSLWIG 20
   ||||| || |||||
DB 30 TGYIHWVKSHGKSLWIG 49

RESULT 9
US-09-328-296-7
; Sequence 7, Application US/09328296
; Patent No. 6946129
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
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; CURRENT APPLICATION NUMBER: US/09/328,296
; CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-328-296-7

Query Match 74.1%; Score 63; DB 2; Length 114;
Best Local Similarity 65.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXKXQSPKSLWIG 20
   ||||| || |||||
DB 30 TGYIHWVKSHGKSLWIG 49

RESULT 10
US-09-698-705-8
; Sequence 8, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koeppe, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P1777r1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 8
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-698-705-8

Query Match 74.1%; Score 63; DB 2; Length 121;
Best Local Similarity 65.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXKXQSPKSLWIG 20
   ||||| || |||||
DB 30 TGYIHWVKSHGKSLWIG 49

RESULT 11
US-09-257-069-2
; Sequence 2, Application US/09257069
; Patent No. 6348580
; GENERAL INFORMATION:
; APPLICANT: Medical & Biological Laboratories Co., Ltd.
; TITLE OF INVENTION: Monoclonal Antibody Specific for
; TITLE OF INVENTION: Phosphatidylinositol-3,4,5-Triphosphate
; FILE REFERENCE: M3-008-US
; CURRENT APPLICATION NUMBER: US/09/257,069
; CURRENT FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: JP 1998-252921
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-257-069-2
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Query Match 74.1%; Score 63; DB 2; Length 124;
 Best Local Similarity 65.0%; Pred. No. 0.0016;
 Matches 13; Conservative 0; Mismatches 7; Indels 7; Gaps 0;

QY 1 TGYVXXXXXQSPKSLWIG 20
 DB 30 TGYVHWVKQSHGKSLWIG 49

RESULT 12
 US-10-007-790-2
 ; Sequence 2, Application US/10007790
 ; Patent No. 6818408
 ; GENERAL INFORMATION:
 ; APPLICANT: Medical & Biological Laboratories Co., Ltd.
 ; TITLE OF INVENTION: Monoclonal Antibody Specific for
 ; TITLE OF INVENTION: Phosphatidylinositol-3,4,5-trisphosphate
 ; FILE REFERENCE: M3-008-US
 ; CURRENT APPLICATION NUMBER: US/10/007,790
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US/09/257,069
 ; PRIOR FILING DATE: 1999-02-24
 ; PRIOR APPLICATION NUMBER: JP 1998-252921
 ; PRIOR FILING DATE: 1998-09-07
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-007-790-2

Query Match 74.1%; Score 63; DB 2; Length 124;
 Best Local Similarity 65.0%; Pred. No. 0.0016;
 Matches 13; Conservative 0; Mismatches 7; Indels 7; Gaps 0;

QY 1 TGYVXXXXXQSPKSLWIG 20
 DB 30 TGYVHWVKQSHGKSLWIG 49

RESULT 13
 US-09-471-276-850
 ; Sequence 850, Application US/09471276
 ; Patent No. 6822072
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6822072
 ; FILE REFERENCE: GENSET.025CPI
 ; CURRENT APPLICATION NUMBER: US/09/471,276
 ; CURRENT FILING DATE: 1999-12-21
 ; EARLIER APPLICATION NUMBER: 09/057,719
 ; EARLIER FILING DATE: 1998-04-09
 ; EARLIER APPLICATION NUMBER: 09/069,047
 ; EARLIER FILING DATE: 1998-04-28
 ; EARLIER APPLICATION NUMBER: PCT/IB99/00712
 ; EARLIER FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 1622
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 850
 ; LENGTH: 140
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: -26...-1
 US-09-471-276-850

Query Match 74.1%; Score 63; DB 2; Length 140;
 Best Local Similarity 63.2%; Pred. No. 0.0019;

Matches 12; Conservative 0; Mismatches 7; Indels 7; Gaps 0;
 QY 2 GYVXXXXXQSPKSLWIG 20
 DB 57 GYVSWIRQSPKGLWIG 75

RESULT 14
 US-09-698-705-13
 ; Sequence 13, Application US/09698705
 ; Patent No. 6824780
 ; GENERAL INFORMATION:
 ; APPLICANT: Devaux, B.
 ; APPLICANT: Keller, G.
 ; APPLICANT: Koepfen, H.
 ; APPLICANT: Lasky, L.
 ; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
 ; FILE REFERENCE: P177RI
 ; CURRENT APPLICATION NUMBER: US/09/698,705
 ; CURRENT FILING DATE: 2000-10-27
 ; PRIOR APPLICATION NUMBER: US 60/162,558
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: US 60/182,872
 ; PRIOR FILING DATE: 2000-02-16
 ; NUMBER OF SEQ ID NOS: 25
 ; SEQ ID NO 13
 ; LENGTH: 222
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: sequence is chimeric mouse/human
 US-09-698-705-13

Query Match 74.1%; Score 63; DB 2; Length 222;
 Best Local Similarity 65.0%; Pred. No. 0.0031;
 Matches 13; Conservative 0; Mismatches 7; Indels 7; Gaps 0;

QY 1 TGYVXXXXXQSPKSLWIG 20
 DB 30 TGYVHWVKQSHGKSLWIG 49

RESULT 15
 US-08-230-843-4
 ; Sequence 4, Application US/08230843
 ; Patent No. 5582826
 ; GENERAL INFORMATION:
 ; APPLICANT: SHIMAMURA, TOSHIRO
 ; APPLICANT: HAMURO, JUNJI
 ; APPLICANT: NAKAZAWA, HARUMI
 ; APPLICANT: KANAYAMA, YUKA
 ; APPLICANT: SUGAMURA, KAZUO
 ; APPLICANT: TAKESHITA, TOSHIKAZU
 ; TITLE OF INVENTION: IMMUNOSUPPRESSANT
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/230,843
 ; FILING DATE: 21-APR-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: JP 094491/1993
; FILING DATE: 21-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 036065/1994
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5582826man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0674-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-230-843-4

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Query Match      74.1%; Score 63; DB 1; Length 243;
Best Local Similarity 65.0%; Pred. No. 0.0035;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      1 TGYXXXXXXQSPKXSLWIG 20
      ||||| || |||||
Db     152 TGYMHWVKQSHVKSLEWIG 171

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Search completed: October 18, 2006, 19:50:49
Job time : 25.1237 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2006, 20:43:15 ; Search time 14.3299 Seconds
(without alignments)
112.851 Million cell updates/sec

Title: US-10-620-621-1

Perfect score: 85

Sequence: 1 TGYXXXXQSPKSLWIG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 300827 seqs, 80857292 residues

Total number of hits satisfying chosen parameters: 300827

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	79	92.9	470	6	US-10-526-741-12	Sequence 12, Appl
2	79	92.9	470	7	US-11-414-676-12	Sequence 12, Appl
3	64	75.3	120	7	US-11-221-902-18	Sequence 18, Appl
4	64	75.3	447	7	US-11-221-902-8	Sequence 8, Appl
5	63	74.1	139	7	US-11-221-902-14	Sequence 14, Appl
6	63	74.1	447	7	US-11-221-902-4	Sequence 4, Appl
7	63	74.1	447	7	US-11-221-902-6	Sequence 6, Appl
8	63	74.1	450	7	US-11-221-902-2	Sequence 2, Appl
9	61	71.8	491	7	US-11-293-697-4290	Sequence 4290, Ap
10	60	70.6	117	6	US-10-972-236-4	Sequence 4, Appl
11	59	69.4	78	1	US-09-784-950-85	Sequence 85, Appl
12	59	69.4	92	1	US-09-784-950-86	Sequence 86, Appl
13	59	69.4	92	1	US-09-784-950-87	Sequence 87, Appl
14	59	69.4	116	7	US-11-241-154-6	Sequence 6, Appl
15	59	69.4	124	7	US-11-111-688-1	Sequence 1, Appl
16	59	69.4	126	7	US-11-111-688-55	Sequence 55, Appl
17	59	69.4	128	7	US-11-094-132-67	Sequence 67, Appl
18	59	69.4	139	7	US-11-413-563-2	Sequence 2, Appl
19	59	69.4	190	1	US-09-784-950-33	Sequence 33, Appl
20	59	69.4	202	1	US-09-784-950-31	Sequence 31, Appl
21	59	69.4	205	1	US-09-784-950-23	Sequence 23, Appl
22	58	68.2	76	7	US-11-267-860-35	Sequence 35, Appl
23	58	68.2	98	7	US-11-221-902-52	Sequence 52, Appl
24	58	68.2	98	7	US-11-221-902-64	Sequence 64, Appl
25	58	68.2	118	6	US-10-981-300-51	Sequence 51, Appl

26	58	68.2	120	7	US-11-221-902-19	Sequence 19, Appl
27	58	68.2	120	7	US-11-221-902-21	Sequence 21, Appl
28	58	68.2	121	7	US-11-211-917-66	Sequence 66, Appl
29	58	68.2	121	7	US-11-211-917-82	Sequence 82, Appl
30	58	68.2	121	7	US-11-211-917-98	Sequence 98, Appl
31	58	68.2	122	7	US-11-211-917-110	Sequence 110, App
32	58	68.2	126	7	US-11-211-917-42	Sequence 42, Appl
33	58	68.2	149	7	US-11-355-464-13	Sequence 13, Appl
34	58	68.2	149	7	US-11-355-464-16	Sequence 16, Appl
35	58	68.2	150	7	US-11-324-769-14	Sequence 14, Appl
36	58	68.2	157	7	US-11-267-860-67	Sequence 67, Appl
37	58	68.2	247	6	US-10-539-402-10	Sequence 10, Appl
38	58	68.2	247	7	US-11-221-902-10	Sequence 10, Appl
39	58	68.2	447	7	US-11-221-902-12	Sequence 12, Appl
40	58	68.2	447	7	US-11-221-902-84	Sequence 84, Appl
41	58	68.2	466	7	US-11-211-917-70	Sequence 70, Appl
42	58	68.2	466	7	US-11-211-917-86	Sequence 86, Appl
43	58	68.2	471	7	US-11-211-917-46	Sequence 46, Appl
44	57	67.1	95	7	US-11-267-860-53	Sequence 53, Appl
45	57	67.1	96	7	US-11-267-860-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-10-526-741-12
; Sequence 12, Application US/10526741
; Publication No. US20060167232A1
; GENERAL INFORMATION:

; APPLICANT: ABURATANI, Hiroyuki
; APPLICANT: MIDORIKAWA, Yutaka
; APPLICANT: NAKANO, Kiyotaka
; APPLICANT: OHIZUMI, Iwao
; APPLICANT: ITO, Yukio
; APPLICANT: TOKITA, Susumu
; TITLE OF INVENTION: ANTIBODY AGAINST SOLUBLE N-TERMINAL PEPTIDE OR C-TERMINAL PEPTIDE
; FILE REFERENCE: PRESENT IN BLOOD

; CURRENT APPLICATION NUMBER: US/10/526,741
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: PCT/JP02/08999
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 12
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mouse-human
; OTHER INFORMATION: chimeric antibody (MIE07 H chain)

US-10-526-741-12

Query Match 92.9%; Score 79; DB 6; Length 470;

Best Local Similarity 75.0%; Pred.No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGYXXXXQSPKSLWIG 20
|||||
Db 49 TGYMHVWKQSPKSLWIG 68
|||||

RESULT 2

US-11-414-676-12
; Sequence 12, Application US/11414676
; Publication No. US20060188510A1
; GENERAL INFORMATION:
; APPLICANT: ABURATANI, Hiroyuki
; APPLICANT: MIDORIKAWA, Yutaka
; APPLICANT: NAKANO, Kiyotaka
; APPLICANT: OHIZUMI, Iwao
; APPLICANT: ITO, Yukio

; APPLICANT: TOKITA, Susumu
; TITLE OF INVENTION: ANTIBODY AGAINST SOLUBLE N-TERMINAL PEPTIDE OR C-TERMINAL PEPTIDE
; TITLE OF INVENTION: PRESENT IN BLOOD
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/414,676
; CURRENT FILING DATE: 2006-04-28
; PRIOR APPLICATION NUMBER: US/10/526,741
; PRIOR FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: PCT/JP02/08999
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mouse-human
; OTHER INFORMATION: chimeric antibody (M1E07 H chain)
US-11-414-676-12

Query Match 92.9%; Score 79; DB 7; Length 470;

Best Local Similarity 75.0%; Pred. No. 4.le-06;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TGYXXXXQSPKSLWIG 20

Db 49 TGYMHVVKSPGQGLEWIG 68

RESULT 3

US-11-221-902-18

; Sequence 18, Application US/11221902

; Publication No. US20060088522A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT

; FILE REFERENCE: 040000-0317285

; CURRENT APPLICATION NUMBER: US/11/221,902

; CURRENT FILING DATE: 2005-09-09

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 18

; LENGTH: 120

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody

; OTHER INFORMATION: sequences

US-11-221-902-18

Query Match

Best Local Similarity 75.3%; Score 64; DB 7; Length 120;

Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYXXXXQSPKSLWIG 20

Db 30 TGYMHVVKSPGQGLEWIG 49

RESULT 4

US-11-221-902-8

; Sequence 8, Application US/11221902

; Publication No. US20060088522A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT

; FILE REFERENCE: 040000-0317285

; CURRENT APPLICATION NUMBER: US/11/221,902

; CURRENT FILING DATE: 2005-09-09

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 8

; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
; OTHER INFORMATION: sequences
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(120)
; OTHER INFORMATION: heavy chain variable region
US-11-221-902-8

Query Match

Best Local Similarity 75.3%; Score 64; DB 7; Length 447;

Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYXXXXQSPKSLWIG 20

Db 30 TGYMHVVKSPGQGLEWIG 49

RESULT 5

US-11-221-902-14

; Sequence 14, Application US/11221902

; Publication No. US20060088522A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT

; FILE REFERENCE: 040000-0317285

; CURRENT APPLICATION NUMBER: US/11/221,902

; CURRENT FILING DATE: 2005-09-09

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 14

; LENGTH: 139

; TYPE: PRT

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)..(19)

; OTHER INFORMATION: leader sequence

; FEATURE:

; NAME/KEY: MATURE PEPTIDE

; LOCATION: (20)..(139)

US-11-221-902-14

Query Match

Best Local Similarity 74.1%; Score 63; DB 7; Length 139;

Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGYXXXXQSPKSLWIG 20

Db 49 TGYMHVVKSPGQGLEWIG 68

RESULT 6

US-11-221-902-4

; Sequence 4, Application US/11221902

; Publication No. US20060088522A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT

; FILE REFERENCE: 040000-0317285

; CURRENT APPLICATION NUMBER: US/11/221,902

; CURRENT FILING DATE: 2005-09-09

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 4

; LENGTH: 447

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody

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; OTHER INFORMATION: sequences
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(120)
; OTHER INFORMATION: heavy chain variable region
US-11-221-902-4

Query Match          74.1%; Score 63; DB 7; Length 447;
Best Local Similarity 65.0%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
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Db 30 TGYMHVVKQSHGKSLWIG 49

RESULT 7
US-11-221-902-6
; Sequence 6, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(120)
; OTHER INFORMATION: heavy chain variable region
US-11-221-902-6

Query Match          74.1%; Score 63; DB 7; Length 447;
Best Local Similarity 65.0%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
   |||||  || |||||
Db 30 TGYMHVVKQSHGKSLWIG 49

RESULT 8
US-11-221-902-2
; Sequence 2, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(120)
; OTHER INFORMATION: heavy chain variable region

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US-11-221-902-2

Query Match          74.1%; Score 63; DB 7; Length 450;
Best Local Similarity 65.0%; Pred. No. 0.0028;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
   |||||  || |||||
Db 30 TGYMHVVKQSHGKSLWIG 49

RESULT 9
US-11-293-697-4290
; Sequence 4290, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4290
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4290

Query Match          71.8%; Score 61; DB 7; Length 491;
Best Local Similarity 61.1%; Pred. No. 0.0069;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 GYXXXXXXQSPKSLWIG 19
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Db 50 GYMWAIQSPDKGLEWI 67

RESULT 10
US-10-972-296-4
; Sequence 4, Application US/10972296
; Publication No. US2006015383A1
; GENERAL INFORMATION:
; APPLICANT: Connex-Gesellschaft zur Optimierung von Forschung und
; APPLICANT: Entwicklung mbH
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: (I.N.S.E.R.M)
; TITLE OF INVENTION: Anti Hepatitis C virus antibody and uses thereof
; FILE REFERENCE: b3030pct
; CURRENT APPLICATION NUMBER: US/10/972,296
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: US/09/744,176
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: ep 98 11 35 95.7
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-972-296-4

Query Match          70.6%; Score 60; DB 6; Length 117;
Best Local Similarity 55.0%; Pred. No. 0.0023;
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
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Db 30 SGYFWTWIRQSPKGLEWI 49

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RESULT 11
US-09-784-950-85
; Sequence 85, Application US/09784950
; Publication No. US20060104974A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Geoffrey C.
; APPLICANT: Blacher, Russell W.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Culwell, Alan R.
; APPLICANT: Green, Larry L.
; APPLICANT: Hales, Joanna
; APPLICANT: Havrilla, Nancy
; APPLICANT: Ivanov, Vladimir E.
; APPLICANT: Lipani, John A.
; APPLICANT: Liu, Qiang
; APPLICANT: Weber, Richard F.
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Abgenix, Inc.
; TITLE OF INVENTION: CD147 BINDING MOLECULES AS THERAPEUTICS
; FILE REFERENCE: ABX-CBL/CD147
; CURRENT APPLICATION NUMBER: US/09/784,950
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: PCT/US99/04583
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 09/034,607
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 09/244,253
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-950-85

Query Match 69.4%; Score 59; DB 1; Length 78;
Best Local Similarity 55.0%; Pred. No. 0.0022;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 1 TGYXXXXXQSPKSLWIG 20
   :|||:|:|:|:|:|:|
Db 11 SGYYWSWIRPPGKLEWIG 30

RESULT 12
US-09-784-950-86
; Sequence 86, Application US/09784950
; Publication No. US20060104974A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Geoffrey C.
; APPLICANT: Blacher, Russell W.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Culwell, Alan R.
; APPLICANT: Green, Larry L.
; APPLICANT: Hales, Joanna
; APPLICANT: Havrilla, Nancy
; APPLICANT: Ivanov, Vladimir E.
; APPLICANT: Lipani, John A.
; APPLICANT: Liu, Qiang
; APPLICANT: Weber, Richard F.
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Abgenix, Inc.
; TITLE OF INVENTION: CD147 BINDING MOLECULES AS THERAPEUTICS
; FILE REFERENCE: ABX-CBL/CD147
; CURRENT APPLICATION NUMBER: US/09/784,950
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: PCT/US99/04583
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 09/034,607
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-950-87

Query Match 69.4%; Score 59; DB 1; Length 78;
Best Local Similarity 55.0%; Pred. No. 0.0022;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 1 TGYXXXXXQSPKSLWIG 20
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Db 11 SGYYWSWIRPPGKLEWIG 30

RESULT 13
US-09-784-950-87
; Sequence 87, Application US/09784950
; Publication No. US20060104974A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Geoffrey C.
; APPLICANT: Blacher, Russell W.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Culwell, Alan R.
; APPLICANT: Green, Larry L.
; APPLICANT: Hales, Joanna
; APPLICANT: Havrilla, Nancy
; APPLICANT: Ivanov, Vladimir E.
; APPLICANT: Lipani, John A.
; APPLICANT: Liu, Qiang
; APPLICANT: Weber, Richard F.
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Abgenix, Inc.
; TITLE OF INVENTION: CD147 BINDING MOLECULES AS THERAPEUTICS
; FILE REFERENCE: ABX-CBL/CD147
; CURRENT APPLICATION NUMBER: US/09/784,950
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: PCT/US99/04583
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 09/034,607
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 09/244,253
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-950-87

Query Match 69.4%; Score 59; DB 1; Length 92;
Best Local Similarity 55.0%; Pred. No. 0.0027;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 1 TGYXXXXXQSPKSLWIG 20
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Db 11 SGYYWSWIRPPGKLEWIG 30

RESULT 14
US-11-241-154-6
; Sequence 6, Application US/11241154
; Publication No. US2006017442A1
; GENERAL INFORMATION:
; APPLICANT: Tibor Keler
; TITLE OF INVENTION: METHOD OF TREATING CD30 POSITIVE LYMPHOMAS
; FILE REFERENCE: MXI-327
; CURRENT APPLICATION NUMBER: US/11/241,154
; CURRENT FILING DATE: 2005-09-30
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; PRIOR APPLICATION NUMBER: 60/615284
; PRIOR FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-241-154-6

Query Match 69.4%; Score 59; DB 7; Length 116;
Best Local Similarity 55.0%; Pred. No. 0.0034; 8; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 TGYXXXXXQSPKSLWIG 20
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Db 30 SGYWSWIRQPPKGLWIG 49

RESULT 15
US-11-111-688-1
; Sequence 1, Application US/11111688
; Publication NO. US20060115486A1
; GENERAL INFORMATION:
; APPLICANT: Pier, Gerald B
; APPLICANT: Kelly-Quintos, Casie A
; APPLICANT: Cavacini, Lisa
; APPLICANT: Rosner, Marshall R
; TITLE OF INVENTION: POLY-N-ACETYL GLUCOSAMINE (PNAG/6PNAG) -BINDING
; FILE REFERENCE: B0801.70300US01
; CURRENT APPLICATION NUMBER: US/11/111,688
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: US 60/564,105
; PRIOR FILING DATE: 2004-04-21
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-111-688-1

Query Match 69.4%; Score 59; DB 7; Length 124;
Best Local Similarity 55.0%; Pred. No. 0.0037; 8; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 TGYXXXXXQSPKSLWIG 20
:|||||
Db 30 SGYWSWIRQPPKGLWIG 49

Search completed: October 18, 2006, 20:58:14
Job time : 14.3299 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 18, 2006, 19:47:09 ; Search time 294.33 Seconds
(without alignments)
103.758 Million cell updates/sec

Title: US-10-620-621-1

Perfect score: 85

Sequence: 1 TGYVXXXXXQSPKSLWIG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Pending Patents AA Main:*
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 - 41: /EMC_Celerra_SIDS3/ptodata/2/paa/US111 COMB.pap.*
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- 44: /EMC_Celerra_SIDS3/ptodata/2/paa/US114 COMB.pap.*
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- 49: /EMC_Celerra_SIDS3/ptodata/2/paa/US604 COMB.pap.*
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- 52: /EMC_Celerra_SIDS3/ptodata/2/paa/US607 COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	80	94.1	20	1	PCT-US96-04206-1	Sequence 1, Appli
2	80	94.1	20	36	US-10-620-621-1	Sequence 1, Appli
3	80	94.1	20	37	US-10-758-397-11	Sequence 11, Appl
4	80	94.1	20	37	US-10-758-397A-11	Sequence 11, Appl
5	79	92.9	20	1	PCT-US96-04206-6	Sequence 6, Appli
6	79	92.9	20	1	PCT-US96-04206-6	Sequence 6, Appli
7	79	92.9	20	34	US-10-468-924-1	Sequence 1, Appli
8	79	92.9	20	34	US-10-468-924A-1	Sequence 1, Appli
9	79	92.9	20	36	US-10-620-621-6	Sequence 6, Appli
10	79	92.9	20	37	US-10-758-397-1	Sequence 1, Appli
11	79	92.9	20	37	US-10-758-397A-1	Sequence 1, Appli
12	79	92.9	103	27	US-09-791-537-11946	Sequence 11946, A
13	79	92.9	105	27	US-09-791-537-8724	Sequence 8724, A
14	79	92.9	111	27	US-09-791-537-14790	Sequence 14790, A
15	79	92.9	112	27	US-09-791-537-14835	Sequence 14835, A
16	79	92.9	115	27	US-09-791-537-14831	Sequence 14831, A
17	79	92.9	138	27	US-09-791-537-14906	Sequence 14906, A
18	79	92.9	137	27	US-09-791-537-77301	Sequence 77301, A
19	79	92.9	470	35	US-10-526-741-12	Sequence 12, Appl
20	74	87.1	97	27	US-09-791-537-61187	Sequence 61187, A
21	71	83.5	255	1	PCT-US01-19110-1826	Sequence 1826, Ap
22	71	83.5	255	1	PCT-US02-36496-1626	Sequence 1626, Ap
23	71	83.5	255	28	US-09-880-748-1626	Sequence 1626, Ap
24	71	83.5	255	32	US-10-293-418-1626	Sequence 1626, Ap
25	71	83.5	255	40	US-11-054-515-1626	Sequence 1626, Ap
26	71	83.5	255	42	US-11-266-444-1626	Sequence 1626, Ap
27	71	83.5	255	52	US-60-723-626-1626	Sequence 1626, Ap
28	71	83.5	255	52	US-60-735-988-1626	Sequence 1626, Ap
29	71	83.5	255	52	US-60-776-665-1626	Sequence 1626, Ap
30	71	83.5	467	39	US-10-961-567A-3	Sequence 3, Appli
31	71	83.5	470	39	US-10-961-567A-9	Sequence 9, Appli
32	70	82.4	119	27	US-09-791-537-135207	Sequence 135207, A
33	68	80.0	671	42	US-11-202-507A-14	Sequence 14, Appl
34	68	80.0	672	29	US-09-900-766-1	Sequence 1, Appli
35	68	80.0	672	42	US-11-202-507A-7	Sequence 7, Appli
36	67	78.8	117	27	US-09-791-537-129898	Sequence 129898, A
37	65	76.5	89	27	US-09-791-537-7370	Sequence 7370, A
38	65	76.5	97	27	US-09-791-537-73709	Sequence 144799, A
39	65	76.5	106	27	US-09-791-537-6277	Sequence 6277, Ap
40	65	76.5	115	27	US-09-791-537-102697	Sequence 102697, A
41	65	76.5	117	27	US-09-791-537-41128	Sequence 41128, A
42	65	76.5	129	33	US-10-312-316-47	Sequence 47, Appl
43	65	76.5	134	27	US-09-791-537-22034	Sequence 22034, A
44	65	76.5	134	27	US-09-791-537-22035	Sequence 22035, A
45	65	76.5	134	27	US-09-791-537-22040	Sequence 22040, A

ALIGNMENTS

RESULT 1
PCT-US96-04206-1
; Sequence 1, Application PC/TUS9604206
; GENERAL INFORMATION:

Query Match 92.9%; Score 79; DB 34; Length 20;
Best Local Similarity 75.0%; Pred. No. 3.6e-06;

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Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
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Db 1 TGYMQWVKQSPKSLWIG 20
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RESULT 12
US-09-791-537-11946
; Sequence 11946, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11946
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-11946

Query Match 92.9%; Score 79; DB 27; Length 103;
Best Local Similarity 75.0%; Pred. No. 1.7e-05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
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Db 49 TGYMQWVKQSPKSLWIG 68
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RESULT 13
US-09-791-537-82724
; Sequence 82724, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82724
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-82724

Query Match 92.9%; Score 79; DB 27; Length 105;
Best Local Similarity 75.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGYXXXXXXQSPKSLWIG 20
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Db 29 TGYMQWVKQSPKSLWIG 48
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RESULT 14
US-09-791-537-14790
; Sequence 14790, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
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; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14790
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-14790

Query Match 92.9%; Score 79; DB 27; Length 111;
Best Local Similarity 75.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 15
US-09-791-537-14835
; Sequence 14835, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14835
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-14835

Query Match 92.9%; Score 79; DB 27; Length 112;
Best Local Similarity 75.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 27 TGYMQWVKQSPKSLWIG 46
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Job time : 295.33 secs
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

US-11-202-507A-14

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Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 30 TGYMHVVKQSPKGLEWIG 49

RESULT 13

US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 80.0%; Score 68; DB 3; Length 672;
Best Local Similarity 65.0%; Pred. No. 0.0072;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCYYXXXXXQSPKSLWIG 20
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DB 30 TGYMHVVKQSPKGLEWIG 49

RESULT 14

US-11-202-507A-7
; Sequence 7, Application US/11202507A
; Publication No. US20060057111A1
; GENERAL INFORMATION:
; APPLICANT: Hedlund, Gunnar
; APPLICANT: Forsberg, Goran
; APPLICANT: Wallen-Ohman, Marie
; TITLE OF INVENTION: TREATMENT OF HYPERPROLIFERATIVE DISEASE WITH SUPERANTIGENS IN
; TITLE OF INVENTION: COMBINATION WITH ANOTHER ANTICANCER AGENT
; FILE REFERENCE: P03024US1
; CURRENT APPLICATION NUMBER: US/11/202,507A
; CURRENT FILING DATE: 2005-08-12
; PRIOR APPLICATION NUMBER: US 60/601,548
; PRIOR FILING DATE: 2004-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Conjugate Protein
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (449)..(672)
; OTHER INFORMATION: Light Chain
US-11-202-507A-7

Query Match 80.0%; Score 68; DB 6; Length 672;
Best Local Similarity 65.0%; Pred. No. 0.0072;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TCYYXXXXXQSPKSLWIG 20
||| |
DB 30 TGYMHVVKQSPKGLEWIG 49

RESULT 15

US-10-312-316-47
; Sequence 47, Application US/10312316
; Publication No. US20040137513A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Hongo, Jo-Anne S.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shelton, David L.
; TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
; FILE REFERENCE: GENENT.0400PC
; CURRENT APPLICATION NUMBER: US/10/312,316
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/238,319
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-316-47

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Best Local Similarity 63.2%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GYXXXXXXQSPKSLWIG 20
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DB 34 GYTWSWIROHPKGLEWIG 52

Search completed: October 18, 2006, 20:55:48
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; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1626
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1626

Query Match 83.5%; Score 71; DB 6; Length 255;
Best Local Similarity 65.0%; Fred. No. 0.00083;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGYXXKXQSPKSLWIG 20
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Db 30 SGYWSVVRQSPKSLWIG 49

RESULT 9
US-11-266-444-1626
; Sequence 1626, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulators
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1626
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1626

Query Match 83.5%; Score 71; DB 6; Length 255;
Best Local Similarity 65.0%; Fred. No. 0.00083;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGYXXKXQSPKSLWIG 20
:|||||
Db 30 SGYWSVVRQSPKSLWIG 49

RESULT 10
US-10-961-567A-3
; Sequence 3, Application US/10961567A
; Publication No. US20050095244A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Hefta, Laura
; APPLICANT: Santoro, Marc
; APPLICANT: Ganguly, Subinay
; TITLE OF INVENTION: FULLY HUMAN ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: 10060 NP
; CURRENT APPLICATION NUMBER: US/10/961,567A
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US 60/510193
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: Patent In version 3.2
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pd17-20H4.9.h4a amino acid sequence
US-10-961-567A-3

Query Match 83.5%; Score 71; DB 5; Length 467;
Best Local Similarity 65.0%; Fred. No. 0.0015;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGYXXKXQSPKSLWIG 20
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Db 49 SGYWSVVRQSPKSLWIG 68

RESULT 11
US-10-961-567A-9
; Sequence 9, Application US/10961567A
; Publication No. US20050095244A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Hefta, Laura
; APPLICANT: Santoro, Marc
; APPLICANT: Ganguly, Subinay
; TITLE OF INVENTION: FULLY HUMAN ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: 10060 NP
; CURRENT APPLICATION NUMBER: US/10/961,567A
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US 60/510193
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 9
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 20H4.9-IgG1 amino acid sequence
US-10-961-567A-9

Query Match 83.5%; Score 71; DB 5; Length 470;
Best Local Similarity 65.0%; Fred. No. 0.0015;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGYXXKXQSPKSLWIG 20
:|||||
Db 49 SGYWSVVRQSPKSLWIG 68

RESULT 12
US-11-202-507A-14
; Sequence 14, Application US/11202507A
; Publication No. US20060057111A1
; GENERAL INFORMATION:
; APPLICANT: Hedlund, Gunnar
; APPLICANT: Forsberg, Goran
; APPLICANT: Wallen-Ohman, Marie
; TITLE OF INVENTION: TREATMENT OF HYPERPROLIFERATIVE DISEASE WITH SUPERANTIGENS IN
; FILE REFERENCE: P03024US1
; CURRENT APPLICATION NUMBER: US/11/202,507A
; CURRENT FILING DATE: 2005-08-12
; PRIOR APPLICATION NUMBER: US 60/601,548
; PRIOR FILING DATE: 2004-08-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 14
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Staphylococcus sp

Best Local Similarity 75.0%; Pred. No. 2.7e-06; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TGYNXXXXXQSPKSLWIG 20
 Db 1 TGYNMQWVKQSPKSLWIG 20

RESULT 5

US-10-758-397-1
 ; Sequence 1, Application US/10758397
 ; Publication No. US200500086341
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen-Vered, et al., Sharon
 ; TITLE OF INVENTION: PARENTERAL FORMULATIONS OF PEPTIDES FOR THE TREATMENT OF SYSTEMIC
 ; FILE REFERENCE: ERYTHEMATOSUS
 ; CURRENT APPLICATION NUMBER: US/10/758,397
 ; CURRENT FILING DATE: 2004-01-14
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide based on CDR of mouse autoantibody
 US-10-758-397-1

Query Match 92.9%; Score 79; DB 5; Length 20;
 Best Local Similarity 75.0%; Pred. No. 2.7e-06;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TGYNXXXXXQSPKSLWIG 20
 Db 1 TGYNMQWVKQSPKSLWIG 20

RESULT 6

US-09-880-748-1626
 ; Sequence 1626, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1626
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-1626

Query Match 83.5%; Score 71; DB 3; Length 255;
 Best Local Similarity 65.0%; Pred. No. 0.00083;
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGYNXXXXXQSPKSLWIG 20
 Db 30 SGYNSWVRQSPKSLWIG 49

RESULT 7

US-10-293-418-1626
 ; Sequence 1626, Application US/10293418
 ; Publication No. US20030223996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 1626
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-293-418-1626

Query Match 83.5%; Score 71; DB 4; Length 255;
 Best Local Similarity 65.0%; Pred. No. 0.00083;
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGYNXXXXXQSPKSLWIG 20
 Db 30 SGYNSWVRQSPKSLWIG 49

RESULT 8

US-11-054-515-1626
 ; Sequence 1626, Application US/11054515
 ; Publication No. US20050255532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
 ; FILE REFERENCE: PF523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816